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Generation of a human induced pluripotent stem cell line (UEFi003-A) carrying heterozygous A673T variant in amyloid precursor protein associated with a reduced risk of Alzheimer's disease

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ABSTRACT

A673T mutation in the amyloid precursor protein (APP) is a rare variant associated with a reduced risk of late-onset Alzheimer's disease (AD) and age-related cognitive decline. The A673T mutation decreases beta-amyloid (A β) production and aggregation in neuronal cultures *in vitro*. Here we have identified a Finnish non-diseased male individual carrying a heterozygous A673T mutation, obtained a skin biopsy sample from him, and generated an iPSC line using commercially available integration-free Sendai virus-based kit. The established iPSC line retained the mutation, expressed pluripotency markers, had a normal karyotype, and differentiated into all three germ layers *in vitro*.

Resource Table:

| | |
|---------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Unique stem cell line identifier | UEFi003-A |
| Alternative name(s) of stem cell line | MADGIC 12B |
| Institution | A.I.Virtanen Institute for Molecular Sciences University of Eastern Finland |
| Contact information of distributor | Šárka Lehtonen, sarka.lehtonen@uef.fi ; sarka.lehtonen@helsinki.fi |
| Type of cell line | iPSC |
| Origin | Human |
| Additional origin info | Age: 58 Sex: male Ethnicity if known: Finnish |
| Cell Source | Skin fibroblasts |
| Clonality | Clonal |
| Method of reprogramming | Sendai virus delivery of <i>OCT-3/4</i> , <i>KLF-4</i> , <i>SOX-2</i> and <i>c-MYC</i> genes |
| Genetic Modification | Yes |
| Type of Modification | Hereditary |
| Associated disease | Protective against Alzheimer's disease |
| Gene/locus | APP (MIM # 104760) located on the chromosome 21q21.3 genotype Chr21: 25,897,620 G > A substitution (rs63750847) |
| Method of modification | NO modification |

| | |
|---------------------------------|--------------------------------------------------------|
| Name of transgene or resistance | NO transgene or resistance |
| Inducible/constitutive system | NO inducible |
| Date archived/stock date | N/A |
| Cell line repository/bank | Registered in hPSCreg.eu |
| Ethical approval | Northern Savo Hospital district (license no. 123/2016) |

1. Resource utility

A β aggregates in the brain are the main hallmark of AD pathology. The A673T mutation in APP reduces the production of A β peptides. The generated line could be used to study the effects of a decreased A β production on neuronal cell function alone and in co-cultures with glial cells.

2. Resource details

APP is an evolutionarily well-conserved type I transmembrane glycoprotein. Its cleavage can produce several different products, including β -amyloid (A β), the accumulation of which has long been considered as the major driving force in AD pathogenesis. The A673T mutation in APP strongly decreases APP cleavage by beta-secretase 1, thus reducing the generation of A β peptides and soluble APP- β (Jonsson

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Table 1
Characterization and validation.

| Classification | Test | Result | Data |
|----------------------------------------------------------------------|--------------------------------------|---------------------------------------------------------------------------------------------------------------|-----------------------|
| Morphology Phenotype | Photography | Visual record of the line: normal | Fig. 1 panel A |
| | Immunocytochemistry | Positive staining of pluripotency markers: Oct4, Nanog, TRA-1-81, SSEA4 | Fig. 1 panel B |
| Genotype | RT-qPCR | Expression of Lin28, Nanog, Sox2 | Fig. 1 panel C |
| | Karyotype (G-banding) and resolution | 46 XY Resolution of 400 band level | Fig. 1 panel E |
| | STR analysis | 13 sites tested, all matched with parental fibroblasts cell line | available with author |
| Identity Mutation analysis | Sequencing | Heterozygous p.A673T in <i>APP</i> | Fig. 1 panel F |
| | Mycoplasma | Mycoplasma testing by PCR. Negative. | Fig. 1 panel D |
| Microbiology and virology Differentiation potential | Embryoid body formation | Positive staining for smooth muscle actin (SMA), beta-III-tubulin (BIIIITub) and α -feto protein (AFP) | Fig. 1 panel G |
| Donor screening (OPTIONAL) | HIV 1 + 2 Hepatitis B, Hepatitis C | N/A | N/A |
| Genotype additional info (OPTIONAL) | Blood group genotyping | N/A | N/A |
| | HLA tissue typing | N/A | N/A |

et al., 2012; Maloney et al., 2014). It is also increasingly recognized that APP plays an important role in normal physiological processes (Brothers et al., 2018). APP is upregulated early in the development, and its cleavage products can regulate neurogenesis, neuronal migration, synapse formation and activity (Nicolas and Hassan, 2014). A β is also known to have antimicrobial activity (Brothers et al., 2018). We have previously reported the generation of an iPSC line from a 65-year old male expressing a rare Chr21: 25,897,620 G > A variant (rs63750847) in the *APP* gene (Lehtonen et al., 2018). Here we have recruited another 58-year-old healthy (without neurological conditions) Finnish male individual carrying the same mutation and generated a new iPSC line (Table 1).

Fibroblasts were reprogrammed using CytoTune™-iPS 2.0 Sendai Reprogramming Kit. The colonies were manually picked and expanded clonally in feeder-free conditions on Matrigel coating. Here, we present the detailed characterization for clone MADGIC 12B. As expected, MADGIC 12B cells were positive for pluripotency markers OCT-4, NANOG, TRA-1-81 (podocalyxin), and SSEA4 as demonstrated by immunocytochemical staining (Fig. 1B). The cells also strongly upregulated *NANOG*, *SOX2*, and *LIN28* and downregulated Sendai virus (*SeV*) gene expression compared to the parental fibroblasts shown by quantitative real-time PCR (Fig. 1C). Chromosomal analysis showed a normal karyotype (Fig. 1E). STR analysis confirmed the identical genetic background of the donor fibroblasts and the iPSC clone (data available from the authors). PCR amplification of *APP* locus followed by Sanger sequencing confirmed the presence of a heterozygous Chr21: 25,897,620 G > A mutation (Fig. 1F). In addition, MADGIC 12B line formed embryoid bodies (EBs) when plated in the ultra-low adherent plate. Immunocytochemical analysis of the EBs was performed after 28 days of culture. It showed a spontaneous differentiation into cell types representative of the three embryonic germ layers, including smooth muscle antibody (SMA)-positive cells (mesoderm), alpha-feto-protein (AFP)-positive cells (endoderm) and beta-III-tubulin (B-III-TUB)-positive cells (ectoderm) (Fig. 1G). A PCR-based mycoplasma detection test was negative (Fig. 1D).

3. Materials and methods

3.1. Generation of induced pluripotent stem cells

Punch skin biopsy was collected from a healthy male individual recruited by Kuopio University Hospital, Finland, after obtaining informed consent. Skin fibroblasts were expanded as described previously (Lehtonen et al., 2018) and transduced using CytoTune™-iPS 2.0 Sendai Reprogramming Kit (Thermo Fisher Scientific) according to the manufacturer's instructions in fibroblast culture medium containing Iscove's DMEM with 20% fetal bovine serum, 1% penicillin–streptomycin and

1% non-essential amino acids (all from Thermo Fisher Scientific). At day 6 post-transduction, fibroblast culture medium was replaced with Essential 6 Medium (E6, Thermo Fisher Scientific) supplemented with 100 ng/ml basic fibroblast growth factor (bFGF; Peprotech). At three weeks post-transduction, individual reprogrammed iPSC colonies were selected based on morphology and re-plated onto Matrigel (growth factor reduced; Corning; 1:200)-coated 24-well plates. Four iPSC clones were further expanded and grown routinely in feeder-free conditions in Essential 8 Medium (Thermo Fisher Scientific) on Matrigel-coated (1:200) 3.5 cm dishes at 37 °C 5% CO₂. The cells were passaged with 0.5 mM EDTA every 4–5 days.

3.2. Genetic analysis

To confirm identical genetic background of the derived clone and parental fibroblasts, thirteen microsatellite loci (D8S1179, D21S11, D16S538, D2S1338, D18S51, VWA_CHR12, FGA_CHR4, D10S1248, D12S391, D4S385a/b, SE33, CSF1PO and HPTRB; Table 2) were analyzed by conventional PCR using MyTaq DNA polymerase (Bioline). Genomic DNA was isolated from the cells using the NucleoSpin Tissue Mini DNA extraction kit (Macherey-Nagel). PCR products were resolved by running electrophoresis for 1.5 h on a 3% agarose gel in TBE buffer. The presence of the A673T mutation was confirmed by PCR and Sanger sequencing performed at the Institute for Molecular Medicine Finland (FIMM), University of Helsinki (primers listed in Table 2, Rev-primer used for sequencing).

3.3. Embryoid body formation

To prove our new iPSC line's ability to differentiate to all three germ layers spontaneously, we performed an embryoid body (EB) formation assay. iPSCs colonies were detached by using ReLeSR passaging reagent (StemCell Technologies) and cultured in suspension for two weeks in ultra-low adherent 6-well plates (Corning) containing DMEM medium supplemented with 20% Serum replacement and 1% Penicillin–Streptomycin (Thermo Fisher Scientific). Afterwards, EBs were re-plated onto Matrigel-coated 24-well plates and left to differentiate for two more weeks. The scale bar for EBs in suspension is 200 μ m.

3.4. Quantitative RT-PCR and immunocytochemistry

RNA was extracted using the RNeasy Mini kit (Qiagen), and quantitative RT-PCR was done using commercially available Taqman probes (Table 2) according to the manufacturer's instructions. For immunocytochemistry, plated iPSCs and EBs were fixed in 4% formaldehyde for 20 min at room temperature and stained with the primary antibodies (Table 2) diluted in 5% normal goat serum in PBS with

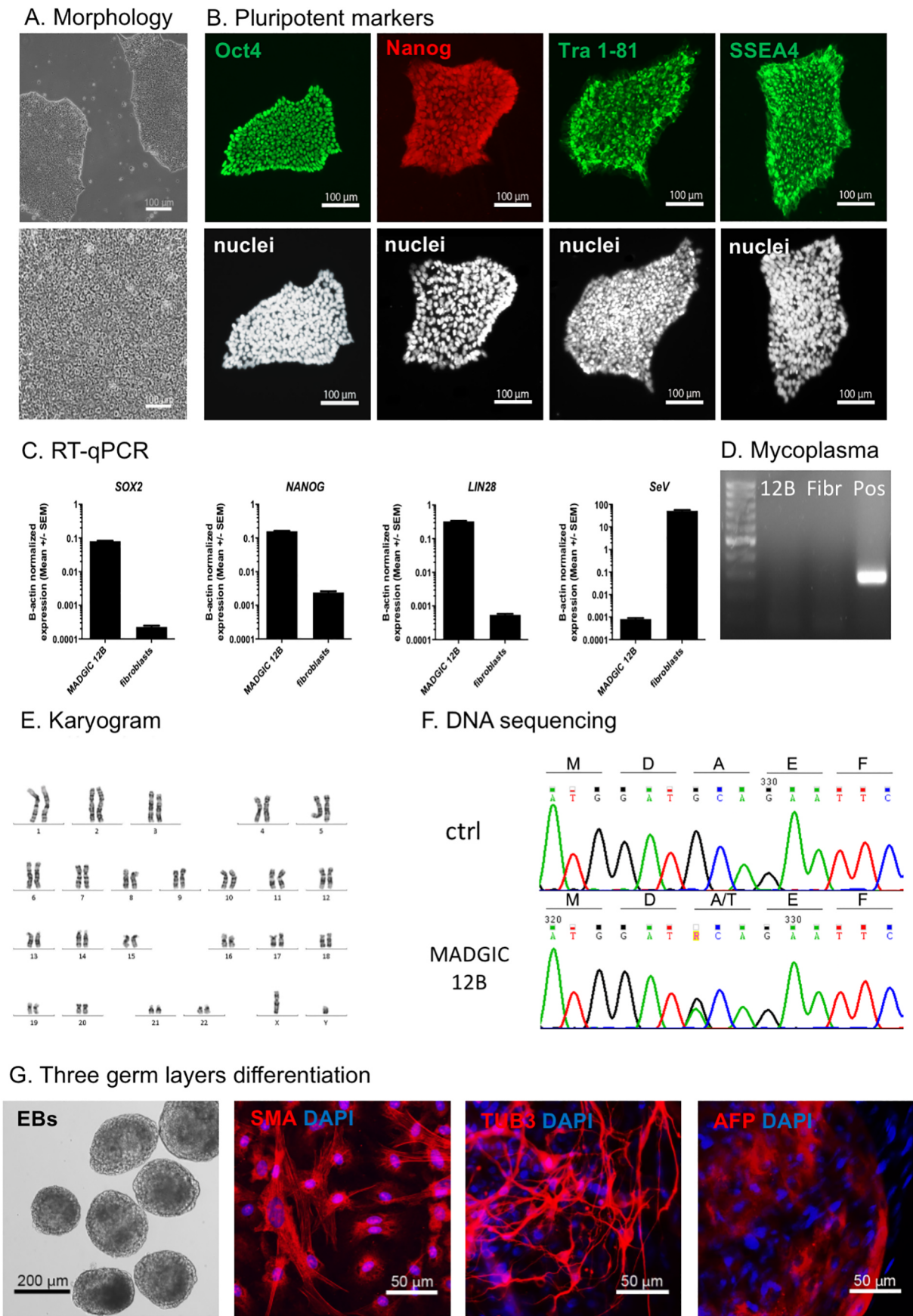


Table 2
Reagents details.

| Antibodies used for immunocytochemistry | | | |
|-----------------------------------------|----------------------------------|--------------------------------------------------------|------------------------------------------------|
| | Antibody | Dilution | Company Cat # and RRID |
| Pluripotency Markers | Mouse anti-Oct4 | 1:400 | EMD Millipore; cat. MAB4401; RRID:AB_2167852 |
| | Goat anti-Nanog | 1:200 | R&D Systems; cat. AF1997; RRID:AB_355097 |
| | Mouse anti-TRA-1-81 | 1:400 | EMD Millipore; cat. MAB4381; RRID:AB_177638 |
| | Mouse anti-SSEA4 | | EMD Millipore; cat. MAB4304; RRID:AB_177629 |
| Differentiation Markers | Mouse anti-SMA | 1:300 | Sigma-Aldrich; cat. A5228; RRID:AB_262054 |
| | Mouse anti-B-III-tubulin | 1:1000 | Covance; cat. MMS-435P; RRID:AB_2313773 |
| | Mouse anti-AFP | 1:300 | Sigma-Aldrich; cat. A8452; RRID:AB_258392 |
| | Goat anti-mouse Alexa Fluor 488 | 1:300 | Molecular Probes; cat. A11001; RRID:AB_2534069 |
| Secondary antibodies | Goat anti-mouse Alexa Fluor 568 | 1:300 | Molecular Probes; cat. A11004; RRID:AB_2534072 |
| | Donkey anti-goat Alexa Fluor 568 | | Molecular Probes; cat. A11057; RRID:AB_142581 |
| Primers | | | |
| | Target | Forward/Reverse primer (5'-3') | |
| Mutation analysis/sequencing | APP | TGGCAAGACAAACAGTAGTGG/ CTTGCCACCTCTCAACCAG (453 bp) | |

Table 2 (continued)

| Antibodies used for immunocytochemistry | | | |
|-----------------------------------------|--------------------|--------------------------------------------------------------------------------|------------------------|
| | Antibody | Dilution | Company Cat # and RRID |
| STR analysis | D8S1179 | GTATCGTATCCCATTTGCGTG/ CGCCTTTGCGCTGAGTTTTG (197–249 bp) | |
| | D21S11 | TGTGAGTCAATTCCCAAGTG/ CACTGAGAAGGGAGAAACACTG (286–344 bp) | |
| | D16S538 | GTTCCCATTTTTATATGGGAGC/ TTTACGTTTGTGTGTGCATCTG (165–213 bp) | |
| | D2S1338 | GAAGCCAGTGGATTTGGAAAC/ TCCTACCAGAATGCCAGTCC (206–274 bp) | |
| | D18S51 | CATGCCACTGCACCTTCACTC/ AAGGTGGACATGTTGGCTTC (169–256 bp) | |
| | VWA_CHR12 | CCCTAGTGGATGATAAGAATAATCAGTATG/ GGACAGATGATAAATACATAGGATGGATGG (122–182 bp) | |
| | FGA_CHR4 | TGCCCCATAGGTTTTGAAC/ CTTTGCGCTTCAGGACTTC (266–422 bp) | |
| | D10S1248 | GGAATAAGTGCAGTGCCTGG/ ACCAATCTGGTCACAAACAT (227–271 bp) | |
| | D12S391 | AACAGGATCAATGGATGCAT/ TGGCTTTTAGACCTGGACTG (209–253 bp) | |
| | DYS385 a/b | AGCATGGGTGACAGAGCTA/ TGGGATGCTAGGTAAGCTG (352–436 bp) | |
| | SE33 | AATCTGGGCGACAAGAGTGA/ ACATCTCCCTACCGCTATA (197–343 bp) | |
| | CSF1PO | AACCTGAGTCTGCCAAGGACTAGC/ TTCCACACACCACTGGCCATCTTC (287–331 bp) | |
| | HPRTB | ATGCCACAGATAATACACATCCCC/ CTCTCCAGAATAGTTAGATGTAGG (259–303 bp) | |
| | Mycoplasma testing | TGCACCATCTGTCACTCTGTAAACCTC/ GGGAGCAAACAGGATTAGATACCCCT (271 bp) | |
| Primers | Target | Company | |
| Pluripotency Markers | Nanog | Thermo Fisher Scientific; cat. Hs02387400_g1 | |
| | Lin28 | Thermo Fisher Scientific; cat. Hs00702808_s1 | |
| Housekeeping Genes (qPCR) | Sox2 | Thermo Fisher Scientific; cat. Hs01053049_s1 | |
| | ACTB | Thermo Fisher Scientific; cat. 4326315E | |
| Sendai virus | SeV | Thermo Fisher Scientific; cat. Mr04269880_mr | |

the exception of Nanog antibody, which was diluted in 0.1% bovine serum albumin in PBS, at 4 °C overnight. For the staining of nuclear markers, cells were permeabilized with 0.2% Triton X-100. The following day, the secondary antibodies (1:300 dilution, [Table 2](#)) were added for 1 h at room temperature. Images were taken using a Zeiss AXIO microscope. Scale bars are 100 µm for iPSCs and 50 µm for plated EBs.

3.5. Karyotype analysis

Karyotyping was performed using Giemsa (G-banding) staining as described ([Lehtonen et al., 2018](#)). Twenty metaphases were analyzed. The analyses were performed at the Yhtyneet Medix laboratoriot,

Finland (<http://www.yml.fi/>).

3.6. *Mycoplasma* testing

The absence of mycoplasma contamination was confirmed by PCR reaction targeting mycoplasma-specific 16S ribosomal RNA (primer sequence listed in Table 2) followed by gel electrophoresis.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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